

IN THE CLAIM

Please amend claims 1, 3, 5, 7, 15-18, 20, 22, 24 and 26 and cancel claim 25 without disclaiming its subject matter to read as follows:.

1 1. (Currently Amended) A method for determining gender from a human DNA sample,
2 said method comprising:

3 providing a human DNA sample, said DNA sample containing X chromosomal material
4 and potentially containing Y chromosomal material;

5 ~~selecting at least one locus from a non-combining X-Y homologous region, said region~~
6 ~~containing a monomorphic *Alu* insertion in one of the X chromosome and the Y chromosome;~~

7 amplifying ~~the selected locus~~ at least one locus containing one of *AluSTYa* locus and
8 *AluSTXa* locus of the DNA sample in an amplification reaction, wherein the product of the
9 reaction is a mixture of amplified alleles from the amplified locus present in the sample; and

10 determining the gender of the DNA sample by evaluating the amplified alleles in terms of
11 size and number.

1 2. (Original) The method of claim 1, wherein said amplification reaction is a polymerase
2 chain reaction.

1 3. (Currently Amended) The process of claim 2, wherein ~~the amplification step~~
2 ~~comprises an amplification of~~ said at least one locus is ~~[[an]]~~ *AluSTYa* locus.

1 4. (Original) The method of claim 3, wherein said amplification step comprises the step
2 of using primer pairs containing the following sequences:

3 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

4 and

5 Reverse 5'- CCTTTTCATCCAACCTACCACTGA -3' (SEQ ID NO: 2).

1 5. (Currently Amended) The process of claim 2, wherein ~~the amplification step~~
2 ~~comprises an amplification of~~ said at least one locus is ~~[[an]]~~ *AluSTXa* locus.

1 6. (Original) The method of claim 5, wherein said amplification step comprises the step
2 of using primer pairs containing the following sequences:

3 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

4 and

5 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 7. (Currently Amended) The process of claim 2, wherein said amplification step
2 comprises an amplification of ~~[[an]]~~ *AluSTXa* locus and an amplification of ~~[[an]]~~ *AluSTYa*.

1 8. (Original) The method of claim 7, wherein said amplification step comprises the step
2 of using primer pairs containing the following sequences:

3 for said amplification of the *AluSTXa* locus, 5'- TGAAGAAATTCAGTTCATAGCTTGT
4 -3' (SEQ ID NO: 3) and 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and
5 for said amplification of the *AluSTYa*, 5'- CATGTATTTGATGGGGATAGAGG -3'
6 (SEQ ID NO: 1) and 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 9. (Original) The method of claim 2, wherein at least one primer of each pair has a
2 fluorescent label covalently attached thereto.

1 10. (Original) The method of claim 1, wherein the sizes of the amplified alleles are
2 evaluated by fragment resolution on an agarose gel.

1 11. (Original) The method of claim 10, wherein the sizes of the amplified alleles are
2 evaluated by comparison with a size standard such that:

3 for a Y insertion *AluSTYa* an *Alu* filled site for Y chromosome has size approximately
4 528 base pairs and an empty site for X chromosome has size approximately 199 base pairs; or

5 for an X insertion *AluSTXa* an *Alu* filled site for X chromosome has size approximately
6 878 base pairs and an empty site for Y chromosome has size approximately 556 base pairs.

1 12. (Original) The method of claim 1, wherein male gender is characterized by presence
2 of two DNA fragments and female gender is characterized by presence of one DNA fragment,
3 for amplified loci.

1 13. (Withdrawn) A primer pair adapted for assaying a Y insertion in a sex determination
2 of human cells, each primer pair having the sequence selected from, or constituting a subset of,
3 the group consisting of:

4 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5 and

6 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 14. (Withdrawn) A primer pair adapted for assaying an X insertion in a sex
2 determination of human cells, each primer having the sequence selected from, or constituting a
3 subset of, the group consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 15. (Currently Amended) A kit adapted for analyzing alleles of *AluSTY*a locus on
2 an Y chromosome, said kit comprising a primer pair, each primer of the primer pair having the
3 sequence selected from, or constituting a subset of, the group consisting of:

4 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5 and

6 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 16. (Currently Amended) A kit adapted for analyzing alleles of *[[an]] AluSTXa* locus on
2 a X chromosome, said kit comprising a primer pair wherein each primer of the primer pair has
3 the sequence selected from, or constituting a subset of, the group consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 17. (Currently Amended) A kit for determining gender from a sample, comprising:
2 polymerase chain reaction ~~regents~~reagents comprising a polymerase and buffer; and
3 a pair of primers to amplify at least one locus of *AluSTYa* locus and *AluSTXa* locus in a
4 non-combining X-Y homologous region of the DNA sample, said locus containing a
5 monomorphic *Alu* insertion.

1 18. (Currently Amended) The kit of claim 17, wherein said at least one locus is *[[an]]*
2 *AluSTYa* locus.

1 19. (Withdrawn) The kit of claim 18, wherein said primer pairs containing the following
2 sequences:

3 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

4 and

Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

20. (Currently Amended) The kit of claim 17, wherein said at least one locus is [[an]]
AluSTXa locus.

21. (Withdrawn) The kit of claim 20, wherein said primer pairs containing the following
sequences:

Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

and

Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

22. (Currently Amended) The kit of claim 17, wherein said at least one locus comprises
[[an]] *AluSTYa* locus and an *AluSTXa* locus.

23. (Withdrawn) The kit of claim 22, wherein said pair of primers comprises:
a first primer pair, wherein each primer of the first primer pair has the sequence selected
from, or constituting a subset of, the group consisting of:

Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

and

Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and

7 a second primer pair, wherein each primer of the second primer pair has the sequence
8 selected from, or constituting a subset of, the group consisting of:

9 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

10 and

11 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 24. (Currently Amended) A method for quantitating male DNA in a sample, said method
2 comprising the steps of:

3 amplifying ~~[[a]]~~ at least one locus of *AluSTYa* and *AluSTXa* in the sample by a
4 polymerase chain reaction, wherein said locus is in a non-combining X-Y homologous region
5 and contains a monomorphic *Alu* insertion;

6 detecting the product of the amplified locus; and

7 comparing the detected result with a result of standard male DNA to quantitate DNA in a
8 sample.

1 25. (Canceled)

1 26. (Currently Amended) The method of ~~claim 25~~ claim 24, wherein said amplification
2 step comprises the step of using primer pairs containing at least one of the following pair of
3 sequences:

4 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3) and

- 5 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and
6 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1) and
7 5'- CCTTTTCATCCAACCTACCACTGA -3' (SEQ ID NO: 2).